SEQUENCE LISTING

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<110> Valenzuela et al.
<120> DORSAL TISSUE AFFECTING FACTOR AND COMPOSITIONS
<130> REG132-B1
<140> Not Yet Known
<141> Filed Herewith
<150> 09/167,874
<151> 1998-10-07
<150> 08/485,721
<151> 1995-07-06
<150> 08/392,935
<151> 1995-09-22
<150> PCT/US93/08326
<151> 1993-09-02
<150> 07/957,401
<151> 1992-10-06
<150> 07/950,410
<151> 1992-09-23
<150> 07/939,954
<151> 1992-09-03
<160> 22
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Val	Leu	ı Gly	7 Leu 20		, Ala	Thr	Pro	Ala 25	-	Gly	/ Gln	. His	30		His	
			Ala					Leu					Leu		gaa Glu	144
		Asp			ttt Phe		Pro					Leu				192
	Leu				ctc Leu 70						Pro					240
					gac Asp											288
					gcg Ala											336
tcg Ser	ggg Gly	gcc Ala 115	atg Met	ccg Pro	agc Ser	gag Glu	atc Ile 120	aaa Lys	ggg Gly	cta Leu	gag Glu	ttc Phe 125	tcc Ser	gag Glu	ggc Gly	384
ttg Leu	gcc Ala 130	cag Gln	ggc Gly	aag Lys	aag Lys	cag Gln 135	cgc Arg	cta Leu	agc Ser	aag Lys	aag Lys 140	ctg Leu	cgg Arg	agg Arg	aag Lys	432
tta Leu 145	cag Gln	atg Met	tgg Trp	ctg Leu	tgg Trp 150	tcg Ser	cag Gln	aca Thr	ttc Phe	tgc Cys 155	ccc Pro	gtg Val	ctg Leu	tac Tyr	gcg Ala 160	480
tgg Trp	aac Asn	gac Asp	ctg Leu	ggc Gly 165	agc Ser	cgc Arg	ttt Phe	tgg Trp	ccg Pro 170	cgc Arg	tac Tyr	gtg Val	aag Lys	gtg Val 175	ggc	528
					cgc Arg											576
					gtg Val			Thr			Arg					624
cgg	cgc	999	ggc.	cag	cgc	tgc	ggc	tgg	att	ccc	atc	cag	tac	ccc	atc	6.72

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Arg Arg Gly Gln Arg Cys Gly Trp Ile Pro Ile Gln Tyr Pro Ile
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                              40
 His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr
   - 50
                          55
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Leu Leu Arg Ser Leu Leu Gly Gly His Tyr Asp Pro Gly Phe Met Ala
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Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Ala Ala Gly
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Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro
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Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
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                                                 125
Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys
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Leu Gln Met Trp Leu Trp Ser Gln Thr Phe Cys Pro Val Leu Tyr Ala
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Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
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Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys

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175

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Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
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gaa	ttgt	gag	cgga	taac	aa t	ttca	.caca	g ga	aaca	igcta	tga	.ccat	gat	tacg	ccaagc	120
tcg	aaat	taa	ccct	cact	aa a	ggga	acaa	a ag	ctgg	agct	сса	ccgc	ggt	ggcg	gccgcc	180.
ttc	ccaa	gta	gagc	ggcg	99 g	ggga	attg	c ga	ccaa	.ctcg	tgo	gcgt	ctt	ctgc	nccgcg	240
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Ile	Arg	Pro	Ala	Pro	Ser	Asp	Asn	Leu	Pro	Leu	Val	Asp	Leu	Ile	Glu	
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His	Pro	Asp	Pro	Ile	Phe	Asp	Pro	Lys	Glu	Lys	Asp	Leu	Asn	Glu	Thr	
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ctg	ctg	cgc	tcg	ctg	ctc	999	ggc	cac	tac	gac	ccg	ggc	ttt	atg	gcc	660
Leu	Leu	Arg	Ser	Leu	Leu	Gly	Gly	His	Tyr	Asp	Pro	Gly	Phe	Met	Ala	
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Thr	Ser	Pro	Pro	Glu	Asp	Arg	Pro	Gly	Gly	Gly	Gly	Gly	Pro	Ala	Gly	-
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			Gly Leu Glu P	tc tcc gag ggc he Ser Glu Gly 25	804					
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*				tg ctg tac gcg al Leu Tyr Ala 160	900					
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aag cca tcc aa Lys Pro Ser Ly 195				cp Arg Cys Gln	1044					
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His Pro Asp Pro Ile Phe Asp Pro Lys Glu Lys Asp Leu Asn Glu Thr 50 55 60

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Thr Ser Pro Pro Glu Asp Arg Pro Gly Gly Gly Gly Pro Ala Gly
85 90 95

Gly Ala Glu Asp Leu Ala Glu Leu Asp Gln Leu Leu Arg Gln Arg Pro 100 105 110

Ser Gly Ala Met Pro Ser Glu Ile Lys Gly Leu Glu Phe Ser Glu Gly
115 120 125

Leu Ala Gln Gly Lys Lys Gln Arg Leu Ser Lys Lys Leu Arg Arg Lys 130 135 140

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Trp Asn Asp Leu Gly Ser Arg Phe Trp Pro Arg Tyr Val Lys Val Gly
165 170 175

Ser Cys Phe Ser Lys Arg Ser Cys Ser Val Pro Glu Gly Met Val Cys 180 185 190

Lys Pro Ser Lys Ser Val His Leu Thr Val Leu Arg Trp Arg Cys Gln
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